

Figure 1

A

O:19 serostrain



B

O:19 strain OH4384



C

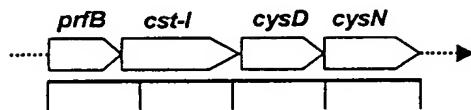
O:19 strain OH4382



Figure 2

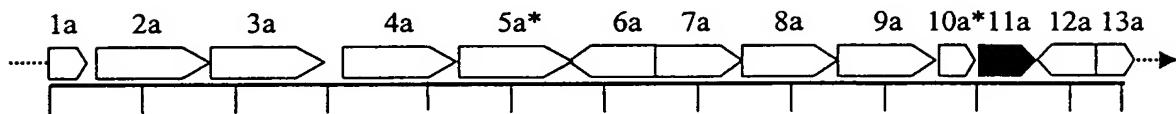
A

OH4384 *cst-I* locus (3.92 kb)



B

OH4382/OH4384 LOS biosynthesis locus (11.47 kb)



NCTC 11168 LOS biosynthesis locus (13.48 kb)

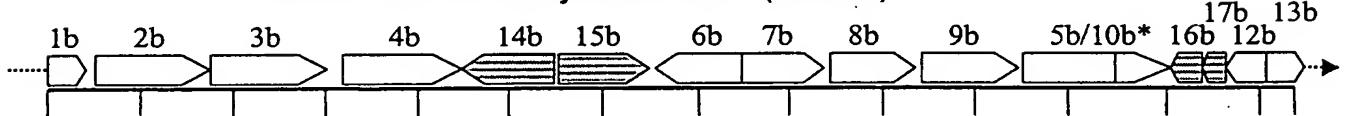


Figure 3

OH4384 O:19 Cst-I 11168 Hi_ORF	MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNCQFYFEDKYYLGK MVKVIAGNGPSLKEIDYSRLPNDFDVFRCNCQFYFEDKYYLGK MTRTRMENELIVSKNMQNIIAGNGPSLKNINYKRLPREYDVFR MSMNINALVCNGNGPSLKNIDYKRLPKQFDVFRCNCQFYFEDR -----	45 45 60 48
OH4384 O:19 Cst-I 11168 Hi_ORF	KAVFYNPILFFEQYYTLKHLIQNQEYETELIMCSNYNQA LENENFVKTFYDYFPDAHLG KAVFTPNFFFEEQYYTLKHLIQNQEYETELIMCSNYNQA LENENFVKTFYDYFPDAHLG KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFLNLP FIESNDFLHQFYNNFPDAKL KYVFFNPFPVFFEQYYTSKKLIQNEEYNIENIVCSTINLEY IDGFQFVDNFELYFSDAFLG -----	105 105 120 108 43
OH4384 O:19 Cst-I 11168 Hi_ORF	MQLIKNNEYEYADIILSSFVNVLGDSELKKIKNVQKLLTQ VQDIDG -----	105 105 120 108 43
OH4384 O:19 Cst-I 11168 Hi_ORF	YDFFKQLKDFNAYFKFHEIYFNQRITSGVYMC AVIALGYKEIYLSGIDFYQN-GSSYAF YDFFKQLKEFNAYFKFHEIYFNQRITSGVYMC AVIALGYKEIYLSGIDFYQN-GSSYAF YEVIENLKEFYAYIKYNEIYFNKRITSGVYMC AIAALGYKTIYL CGIDFYEG-DVIYPF HEI I KKLKDFFAYIKYNEIYNRQRITSGVYMC ATAVALGYKSIIYISGIDFYQDTNNLYAF HYYLNLKLP AFDAYLQYNE LNKRITSGVYMC AVATVMGYKDLYLTGIDFYQEKGNPYAF -----	164 164 179 168 103
OH4384 O:19 Cst-I 11168 Hi_ORF	DTKQKNLKLAPNFKNDNSHYIGHSKNTDI KALEFLEKTYKIKLYCLCPNSLLANFIELA DTKQENLLKLAPDFKNDRSHYIGHSKNTDI KALEFLEKTYKIKLYCLCPNSLLANFIELA EAMSTNIKTIFPGI-K DFKPSNCHSKEYDIE ALKL LKSIYKVNI YALCDDSLANHFPLS DNNKCNLLNKCTGF KNQKF KFNHSMACDL QALDYL MKRYDVNI YSLNSD ----- EYFKLA HHQKENI IKL LPSFSQN KSQSDI HSMEYD LNALYFLQ KHGVN IYC CISP ESPL CNYFPLS -----	224 224 238 224 163
OH4384 O:19 Cst-I 11168 Hi_ORF	PNLN-SNFI I QEK-NNYTKD I LIPSSE AYGKF SKN----- INF KKIK-I KENI YYK PNLN-SNFI I QEK-NNYTKD I LIPSSE AYGKF SKN----- INF KKIK-I KENV YYK ININ-NN FTLEN KHNN SIND ILLTD NTPGV SFYK NQLK ADNK IMLF YNIL HSKDN LIK FPLS D SDFV LSKK PKKY INDI LIPDK YQA QERY YYGK ----- KSR-L KENL HYK PLNN PITFILEEK -K NYTQ DILI PPKF VYKK IGIYS ----- KPR-I YQNL I FR -----	272 272 297 269 209
OH4384 O:19 Cst-I 11168 Hi_ORF	LIKDLLR LPSD I KHYFK GK----- 291 LIKDLLR LPSD I KHYFK GK----- 291 LNKEIA VLKK QTT QRAK ARI QNHLS 322 LIKDL I R LPSD I KHY LKE KYAN KRN 294 LIW DIL LRLP N NDI KHAL KRS KWD --- 231 * ^ ^ ^ ^ * ^ ^ ^ * ^ ^ ^ *	

Figure 4

